geWorkbench

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MAT KC Forum

At a Glance Details

- Version Number and Release Date: 2.6.0.2 February 2015
- Primary audience: Biomedical research practitioners
- Grid Enabled? Yes (5 analytical services)
- Compatibility Level: Silver
- Installation Level: Basic - Wizard or web browser application; minimal technical assistance required
- System Requirements: Refer to the System Requirements section.

CBIIT and NCIP Links

- CBIIT website
- NCIP landing page
- NCI Biomedical Informatics Blog
- NCIP on Twitter @NCI_NCIP

Tool Overview

geWorkbench is a platform for integrated genomics, offering strong capabilities in the analysis and visualization of gene expression, sequence, and protein structure data. It offers direct access to numerous external data sources, including **caArray**, **bioDBNet**, **and BioCarta**, as well as to sequence, molecular interaction, and structural databases. Written in Java for use on the desktop, geWorkbench is open-source and cross-platform, and has an extensible, component-based architecture. geWorkbench is supported by an active development effort.

Installation and Downloads

Downloads

- Download, Install or Upgrade geWorkbench
- geWorkbench plugins
- geWorkbench download area (Columbia)
- Bcell-100 Sample Data

System Requirements

geWorkbench is a desktop application providing access to remote data and analysis services. geWorkbench is downloaded as a self-installing package with support for Windows, Linux and Mac OS X. To achieve reasonable performance when using realistic data sets, a system configuration with at least 4 GB of RAM is recommended.

Forum and Support for geWorkbench

- End User Forum
- Developer Forum
- geWorkbench GForge project archive
- Report a Defect or Request a Feature for geWorkbench at Jira
- Official geWorkbench Bug and Feature Report tracked @ Mantis (Columbia University)
- Application Support

What's New

For news and events, visit What's new for geWorkbench.

Presentations, Demos and Other Materials

- geWorkbench overview at the AACR 2011 Annual Meeting
- geWorkbench Introductory Video (applicable up to geWorkbench 1.7.0) (make sure your speakers are on to play audio)
- geWorkbench Brochures

Documentation and Training

- User tutorials
- Sample Screenshots
- geWorkbench Training Manual
- geWorkbench Project Site
- Installation Requirements
- Installation FAQ
- geWorkbench Known issues
- Developer's Page

geWorkbench Knowledge Base

Visit geWorkbench FAQ and In-depth Articles to find the answers to the most frequently asked questions and develop understanding of how geWorkbench works.

Visit geWorkbench Demos for an in-depth look at operation of geWorkbench.

Refer to geWorkbench Biological Scenarios to see geWorkbench in action and how to apply geWorkbench to your real biological scenarios.

If you still don't know if geWorkbench is for you, review the Case studies to see examples of how geWorkbench could be used in different scenarios.

Refer to geWorkbench Citations for a list of articles about geWorkbench.

Open-source development

- Link to geWorkbench Open Development Code Base (gitub)
- geWorkbench developer's corner

Integration with other tools - caArray

geWorkbench can query for data in an instance of caArray via a Java API. Several operations are supported. You can:

1. Query for experiments, for example by platform or by species
2. Select from which hybridizations in an experiment you wish to download data
3. Download derived (summarized, probeset-level) data that has been parsed into the database. An example is the values loaded from Affymetrix CHP files (created through GCOS/MAS5). geWorkbench does not currently support retrieving or analyzing Affy CEL files directly.